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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/783,807	02/20/2004	Tetsuo Shibuya	JP920030020US1	7767

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EXAMINER	
SMITH, CAROLYN L	

ART UNIT	PAPER NUMBER
1631	

MAIL DATE	DELIVERY MODE
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/783,807	SHIBUYA, TETSUO	
	Examiner	Art Unit	
	Carolyn Smith	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *26 May 2009*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-19* is/are pending in the application.

4a) Of the above claim(s) *4-7,10-12,15-16,18-19* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,8,9,13,14 and 17* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Applicant's amendments and remarks, filed 5/26/09, are acknowledged. Amended claims 1-3, 8-9, 13-14, and 17, filed 5/26/09, are acknowledged. Claims 4-7, 10-12, 15-16, and 18-19 remain withdrawn due to being drawn to non-elected Groups.

Applicant's arguments, filed 5/26/09, have been fully considered but they are not deemed to be persuasive. Rejections and/or objections not reiterated from the previous office actions are hereby withdrawn. The following rejections and/or objections are either reiterated or newly applied. They constitute the complete set presently being applied to the instant application.

Claims herein under examination are 1-3, 8-9, 13-14, and 17.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-3, 8-9, 13-14, and 17 are rejected under 35 U.S.C. 103(a) as being unpatentable over Fujimiya et al. (P/N 5,706,498) in view of Myers et al. (US 6,714,874 B1). This rejection is maintained and reiterated for reasons of record.

Fujimiya et al. describe a computer system, method, program, and computer readable medium for executable screening nucleotide sequences (abstract and Figures 2-4, col. 3, second

and third paragraphs, col. 8, first 2 paragraphs; col. 9, line 45 to col. 10, line 25; col. 12, line 1 to line 18; col. 13, first paragraph), as stated in the preamble of instant claims 1, 8, 13, and 17. Fujimiya et al. describe storing sequence data of genes including target sequence data and key sequence data which exhibit a high degree of similarity (abstract and title and Figure 2 and col. 1, third paragraph; col. 2, fourth paragraph; col. 9, last paragraph) for homology retrieval (col. 2, fourth paragraph) including key memory and target memory (Figure 2) which represent a target and a complementary sequence data storing units, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. describe retrieval databases and preparing a gene probe and analyzing and determining the final sequence of bases by extracting a portion of the gene probe bound to a chromosome (col. 2, second and third paragraph) which represents generating complementary sequence data from a probe sequence and storing such data, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. describe a dynamic operation unit for determining the degree of similarity between the target data and the key data by utilizing base sequence data of each (abstract), grouping homologous sequences, and retrieving the homologous gene sequence (col. 1, fifth paragraph and col. 2, second paragraph) using dynamic programming by summing up points from the starting point of the operation for determining the locally optimal path (i.e. number of adjustments) solution as a whole using insertions, deletions, and substitutions for the first to last combinations of data (col. 2, last paragraph, col. 3, third and fourth paragraphs, and Figures 7a and 7b), altering target data one after another with respect to key data and determining degree of similarity by entering the base sequence data one after another of the target data and storing the sum value of for the sequence data and maximal sum value occurring at the time of operation, classifying the maximal sum values, and determining the order of the

sequence data as an object of extraction (col. 9, lines 21-67; col. 12, lines 32-39; col. 13, lines 1-22), as well as displaying maximal values of each target data in the order of higher degrees of similarity (col. 23, third paragraph), and computation amounting to the number of steps of the basic operations, based on bases in agreement or being replaced (col. 6, third paragraph), and probe binding evaluation (col. 2, second and third paragraphs) which represents an evaluation processing unit for evaluating a binding possibility of the target nucleotide sequence data to the probe sequence via determination of whether the complementary sequence data is similar to a subsequence of the target nucleotide sequence data in descending order of edit distance of binding precision, wherein edit distance is the number of times nucleotides of the subsequence are required to be adjusted to generate the complementary (key) sequence data. Fujimiya et al. describe preparing a gene probe on the basis of the gene having high retrieval accuracy and analyzing and determining the binding possibility of the probe on the involved gene on a chromosome (col. 2, second and third paragraphs), as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. describe a database and retrieving of sequence data using a sequence similar thereto (col. 1, first paragraph) and probe binding analysis and determination (col. 2, second and third paragraphs) and evaluation processing for a user (col. 23, third paragraph) which represents a storage unit for storing the evaluation result for the user in determining probe binding effectiveness and reliability, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. describe using 10 base elements in the sequence data (col. 4, second paragraph) as well as using partial sequences (col. 4, third paragraph). Fujimiya et al. describe a system including storage of data and a similarity degree whereby the score value at the initial condition is set to zero given the condition in which the maximal length α of the sequence is inserted or lost at one time involving

partial sequences as well as setting α to 1 to get a maximal score value (col. 4, last paragraph, and col. 5, and abstract) and performing an operation until reaching a predetermined length of the key or target data and acquiring the maximal value of the sum values with direction selection data (col. 10, line 57 to col. 11, line 43) as well as a constant value to compare sum values (col. 12, lines 1-17) which represents a maximum edit distance storing unit, as stated in instant claims 2, 8, 13, and 17. Fujimiya et al. describe setting a maximal value as a score of the node and applied to the origin and subsequent lattice points until finishing the basic operation and determining the wholly optimal disposition of the three routes (col. 5, last paragraph to col. 6, second paragraph) which represents determining a termination point and a termination-determining unit determining evaluation carried out over maximal (acceptable) edit distance, as stated in instant claims 3, 9, and 14. Fujimiya et al. describe a score value of each route is added, including target-side data and key-side data, as well as outputting sequence data and displaying maximal values and direction selection data (path) (col. 3, third to col. 4, first paragraph; col. 5, second to last paragraph to col. 6, second paragraph; col. 10; col. 11, lines 44-48; col. 20, first paragraph; col. 23, third paragraph; and Figures 7 and 8) which represents reading out each target nucleotide sequence data, complementary sequence data, and each maximum acceptable edit distance, as stated in instant claims 8, 13, and 17. Fujimiya et al. describe the wholly optimal disposition is determined after the basic operations have been made (col. 6, second paragraph and Figures 3-4 and 6) and an interruption signal issued to the microprocessor when the operation is terminated (col. 24, last paragraph) which represents generating a termination signal in response to the determination result, as stated in instant claims 9 and 14. Fujimiya et al. describe using the ability to apply dynamic programming to a local region having approximately

16 bases (col. 7, fourth paragraph). Fujimiya et al. do not describe evaluation is performed in descending order from a first (maximum) edit distance value to a second edit distance value, the second edit distance value being lower than the first (maximum) edit distance value.

Myers et al. describe determining the genomic sequence and screening fragments with their complementary sequences (abstract; col. 2, lines 45-54), identifying a high edit score, inserting a column at the left border of the region, sweeping region from left to right and moving bases leftward if such a move decreases the edit score, repeating the sweeping from right to left, comparing alignments produced in both sweeps and keeping the alignment with the lowest edit score (claim 12; col. 23, 6th paragraph to col. 24, 3rd paragraph) which represents an evaluation is performed in descending order from a first (maximum) edit distance value to a second edit distance value, the second edit distance value being lower than the first (maximum) edit distance value.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to correct alignment within a region as taught by Myers et al. in the screening method of Fujimiya et al. wherein the motivation would have been to assess sequences with an insertion or deficiency of a sequence portion taken into account in a manner that reduces the enormous volume of computation required with dynamic programming, as stated by Fujimiya et al. (col. 2, fifth and sixth paragraphs). One of ordinary skill in the art would have expected success since Fujimiya et al. and Myers et al. both use dynamic programming.

Thus, Fujiymiya et al. in view of Myers et al. make obvious the instant invention.

Applicant summarizes MPEP requirements for a 35 USC 103 rejection. Applicant summarizes Fujimiya et al. and Myers et al. Applicant argues that Myers et al. do not teach anything for the purposes of determining binding possibility of a target sequence to a probe sequence. This statement is found unpersuasive as Fujimiya et al. teach this limitation. Applicant is reminded that a single reference need not teach all of the limitations in a 35 USC 103 rejection. Applicant argues that Myers et al. teach moving left to right within a selected region of bases and "moving bases" within the regions of bases until a lowest edit score alignment is determined for the selected region of bases (col. 24, lines 13-30). Applicant argues that the evaluation for possibility of the target and probe sequence in the instant invention is performed multiple times, in descending order of edit distance value. This statement is found unpersuasive as the claim recites evaluation (singular tense) which can be reasonable interpreted to be a single evaluation. Applicant reiterates arguments several times that Myers et al. do not teach anything for the purposes of determining binding possibility of a target sequence to a probe sequence. It is reiterated that Fujimiya et al. teach this limitation. While it is true that all of the claim limitations must be taught by the prior art, it is also noted that a single reference need not teach all of the limitations in a 35 USC 103 rejection. Applicant argues that neither Fujimiya et al. nor Myers et al. teach determining binding effectiveness and reliability of the probe to the target. This statement is found unpersuasive as Fujimiya et al. describe a database and retrieving of sequence data using a sequence similar thereto (col. 1, first paragraph) and probe binding analysis and determination (col. 2, second and third paragraphs) and evaluation processing for a user (col. 23, third paragraph). It is also noted that determining similarity reasonably encompasses determining effectiveness and reliability of a probe to a target. Applicant argues

that Fujimiya et al. nor Myers et al. do not teach use of distinct units embodied on a tangible computer readable storage medium that execute on a hardware processor. This statement is found unpersuasive as Fujimiya et al. describe a computer system, method, program, and computer readable medium for executable screening nucleotide sequences (abstract and Figures 2-4, col. 3, second and third paragraphs, col. 8, first 2 paragraphs; and col. 13, first paragraph) and various storing unit capabilities (i.e. abstract, claims 1-4, 11-12; col. 9, line 45 to col. 10, line 25; col. 12, line 1 to line 18). Applicant's arguments are deemed unpersuasive for the reasons given above.

Conclusion

No claim is allowed.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The

faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. If you have questions on access to the Private PAIR system, please contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, please call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran, can be reached on (571) 272-0720.

August 31, 2009

/Carolyn Smith/
Primary Examiner
AU 1631